







gggtggcatc ggcgctggtc gtcgtttcat gaacgctctg cagctgttct cccgtgcggt 1020  
 ttccctgggt gacgctgaat ccctggcgca gcacccggca tccatgactc actcctccta 1080  
 cactccggaa gaacgtgcgc actacggcat ctccgaaggc ctggttcgtc tgtctgttgg 1140  
 tctggaagac atcgatgac tgctggcaga cgttcagcag gctctgaagg ctacgccttg 1200  
 ag 1202

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 <212> DNA  
 <213> Artificial sequence

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 cttcccgacc gttgaatacg gcgctgcgtg ctttgtggc gaacaggctg gtcacttcta 180  
 ctcccgatc tccaaccga ccctgaacct gctggaagca cgtatggcat ctctggaagg 240  
 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac 300  
 cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatggtt gtacttttgc 360  
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 cctgca 426

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 <211> 441  
 <212> DNA  
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<400> 5  
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 actttcacct tcccgaccgt tgaatacggc gctgcgtgct ttgctggcga acaggctggt 180  
 cactttact cccgtatctc caaccgacc ctgaacctgc tggaagcacg tatggcatct 240  
 ctggaaggcg gcgaagctgg tctggcgctg gcatctggta tgggcgcgat cacctctacc 300  
 ctgtggaccc tgctgcgtcc gggtgacgaa gttctgctgg gcaacaccct gtatggttgt 360  
 acttttgctt tctgcacca cggtatcggg gaattcggcg ttaaactgcg tcacgtagat 420  
 atggctgacc tgcaggcact g 441

<210> 6  
 <211> 410  
 <212> DNA



<210> 9  
 <211> 383  
 <212> DNA  
 <213> Artificial sequence  
  
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 ttcttcccc cagtacactc tggcacgtca gcagatgtcc cagccgggcg gtatgatcgc 120  
 tttcgaactg aaggggtggca tcggcgctgg tcgtcgtttc atgaacgctc tgcagctggt 180  
 ctcccgctgc gtttccttgg gtgacgtga atccctggcg cagcaccgag catccatgac 240  
 tcaactctcc tacactccgg aagaacgtgc gcaactacggc atctccgaag gcctgggttcg 300  
 tctgtctgtt ggtctggaag acatcgatga tctgctggca gacgttcagc aggctctgaa 360  
 ggctagcgct tgaggatcca cca 383

<210> 10  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 10  
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<210> 11  
 <211> 114  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 11  
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 caggatcacg gtggtgcact ggttcgcgcg gttaccaga ctgctacttt cacc 114

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 <211> 116  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 12  
 gcttcacgca ggttcagggt cgggttgag atacgggagt agaagtgacc agcctgttcg 60  
 ccagcaaagc acgcagcgcc gtattcaacg gtcgggaagg tgaaagtagc agtctg 116

<210> 13  
 <211> 117  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 13  
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 ggcacgggtg ccgggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tcggtttgtc ggtggggctg 1140  
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<210> 29  
 <211> 1197  
 <212> DNA  
 <213> Artificial Sequence

<400> 29  
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 ccgaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggcggggca tttctacagc 180  
 cgcacatcca acccgacct caacctgctg gaagcacgca tggcctcgct ggaaggcggc 240  
 gaggcggggc tggcgctggc ctggggcatg ggggcgatca cgtccacgct gtggacactg 300  
 ctgcgcccgg gtgacgaggt gctgctgggc aacacctgt acggctgcac ctttgcttc 360  
 ctgcaccacg gcacggcga gttcggggtc aagctgcgc atgtggacat ggccgacctg 420  
 caggcaactg aggcggccat gaagcgggc acccggtgta tctatttcga gtgcggggc 480  
 aaccgaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcac caagcacggc 540  
 gcgaccgtgg tggtcgacaa cacctactgc acgccgtacc tgcaacgtcc actggagctg 600  
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 gctggcattg tgggtggcag ccaggcactg gtggaccgta tccgtctgca gggcctcaag 720  
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 gccgctcagc cgcagggtgga gctgatecat taccggggcc tggcgagctt cccgcagtac 900  
 accotggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc 960  
 ggcacgggtg ccgggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tcggtttgtc ggtggggctg 1140  
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<210> 30  
 <211> 1200  
 <212> DNA





Asn Phe Asp Ala Lys Met Val Asp Ala Ile Ile Glu Ala Thr Gly Val  
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Thr Pro Ser Val Asn Gln Ile Glu Arg His Pro Leu Leu Leu Gln Pro  
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Glu Leu Ile Ala His His Lys Ala Lys Asn Ile His Ile Thr Ala Tyr  
195 200 205  
Ser Pro Leu Gly Asn Asn Thr Val Gly Ala Pro Leu Leu Val Gln His  
210 215 220  
Pro Glu Ile Lys Arg Ile Ala Glu Lys Asn Gly Cys Thr Pro Ala Gln  
225 230 235 240  
Val Leu Ile Ala Trp Ala Ile Val Gly Gly His Ser Val Ile Pro Lys  
245 250 255  
Ser Val Thr Pro Ser Arg Ile Gly Glu Asn Phe Lys Gln Val Ser Leu  
260 265 270  
Ser Gln Glu Asp Val Asp Ala Val Ser Lys Leu Gly Glu Gly Ser Gly  
275 280 285  
Arg Arg Arg Tyr Asn Ile Pro Cys Thr Tyr Ser Pro Lys Trp Asp Ile  
290 295 300  
Asn Val Phe Gly Glu Glu Asp Glu Lys Ser Cys Lys Asn Ala Val Lys  
305 310 315 320

Ile Lys

<210> 33  
<211> 972  
<212> DNA  
<213> Artificial sequence

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cgtcatctgg atctggcaaa agtatactct aaccagccgg aagtaggtgc agcaatcaag 180  
gaagctggcg ttaaactgga ggatctgttt atcacttcta aactgtggaa caactccac 240  
cgtccggaac aggtagaacc ggctctggat gatactctga aagaactggg cctggagtat 300  
ctggacctgt acctgatcca ctggccggtg gcatctccgc cggaaggtga tatcactcag 360  
aacctgttcc cgaaagctaa cgataaagaa gtaaaactgg acctggaagt ttctctggta 420  
gacacttgga aagcaatggt aaaactgctg gatactggta aagttaaagc tatcggtggt 480  
tccaactttg acgcaaaaat ggttgacgct atcatcgaag caactggcgt aactccgtct 540  
gttaaccaga tcgaacgtca cccgctgctg ctgcagccag agctgatcgc acaccacaaa 600  
gctaaaaaca tccacatcac cgcatactcc ccgctgggta acaacaccgt aggcgcaccg 660





Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp  
 325 330 335

Leu Val Gly Ser Glu Thr Ala  
 340

<210> 36  
 <211> 1032  
 <212> DNA  
 <213> Artificial Sequence

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 aacgggtttcg ttgggttccca cgttggtgaa cagctgctgg aacacggtta caaagttcgt 120  
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttgga cgctaaatac 180  
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240  
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300  
 tacgacgaag ttgttaccgc ggctatcggg ggtaccctga acgctctgcg tgctgctgct 360  
 gctaccccggt ccgttaaacy tttcgttctg acctcctcca ccgtttccgc tctgatcccg 420  
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatogac 480  
 aaagctaataa cctgcccga atccgacccg cagaaatccc tgtgggtata cgctgcatcc 540  
 aagaaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc aactttcact 600  
 ctgaacgctg tactgcaaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660  
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720  
 ctgatgocac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggtgc 780  
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta ctgctggtac tttcgattgg 840  
 aacaccgttc tggctacctt ccgtaaactg taccgctcca aaaccttccc ggctgacttc 900  
 ccagatcaag gtcaggacct gtctaaatc gacaccgctc cgtccctgga aattctgaaa 960  
 tctctgggtc gccaggttg ggttccatc gaagaatcca tcaaagacct ggttggttcc 1020  
 gaaaccgctt aa 1032

<210> 37  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu  
 1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu





<210> 38  
 <211> 942  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
  
 <400> 38  
 atgggtcctg ctacgttaaa gaattcttct gctacattaa aactaaatac tgggtgcctcc 60  
 attccagtgt tgggtttcgg cacttggcgt tccgttgaca ataacggtta ccattctgta 120  
 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180  
 gaagaagttg gcagggctat taaagattcc ggagtccctc gtgaggaaat ttttattact 240  
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300  
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360  
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420  
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480  
 acgggcaaaa ctaaagccgt tgggtgtctct aatttttcta ttaacaacat taaagaatta 540  
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcatccattg 600  
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg gtattgttgt tgaagcctac 660  
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 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780  
 gttgttctgg ccaaatcggg taatcctgaa agaattgtat ccaattttaa gattttcact 840  
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 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39  
 <211> 313  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 39  
 Met Gly Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn  
 1 5 10 15  
 Thr Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val  
 20 25 30  
 Asp Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr  
 35 40 45  
 Arg His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly  
 50 55 60  
 Arg Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr  
 65 70 75 80

Thr Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn  
85 90 95

Lys Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met  
100 105 110

His Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val  
115 120 125

Leu Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys  
130 135 140

Glu Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys  
145 150 155 160

Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn  
165 170 175

Ile Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr  
180 185 190

Asn Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala  
195 200 205

Phe Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly  
210 215 220

Ser Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala  
225 230 235 240

Lys Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile  
245 250 255

Gln Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile  
260 265 270

Val Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr  
275 280 285

Ile Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met  
290 295 300

Lys Trp Gly Ser Phe Pro Ile Phe Gln  
305 310

<210> 40  
<211> 942  
<212> DNA  
<213> Artificial Sequence

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atcgacgac tgaaagcagg ttaccgtcac atcgacgcag cagcaatcta cctgaacgaa 180  
gaagaagtag gtcgtgcaat caaagactcc ggtgttccgc gtgaagaaat ctttatcact 240  
actaaactgt ggggtactga acagcgtgac ccggaagcag cactgaacaa atctctgaaa 300



<210> 42  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 42

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Gly	Ala	Gln	Ile	Pro	Gln	Ile	Gly	Leu	Gly	Thr	Trp	Gln	Ser	Lys	Glu
			20					25					30		
Asn	Asp	Ala	Tyr	Lys	Ala	Val	Leu	Thr	Ala	Leu	Lys	Asp	Gly	Tyr	Arg
		35					40					45			
His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly	Gln
	50					55					60				
Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr	Thr
65					70					75					80
Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp	Gln
			85					90						95	
Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met	His
			100					105					110		
Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile	Leu
		115					120					125			
Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr	Asn
	130					135					140				
Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys	Thr
145					150					155				160	
Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn	Leu
				165					170					175	
Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala	Asn
		180						185					190		
Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn	Phe
	195						200					205			
Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly	Ser
	210					215					220				
Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala	Lys
225					230					235					240
Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val	Gln
			245						250					255	
Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile	Lys
			260					265					270		
Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala	Ile















cacatcaccg aagcacatgt accaatcata gatacgtacc gggctctgga agaattgtgtt 480  
 gatgaaggct tgattaagtc tattggtgtt tocaactttc aggggaagctt gattcaagat 540  
 ttattacgtg gttgtagaat caagcccggtg gctttgcaaa ttgaacacca tccttatttg 600  
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 caagtattgc ttagatgggc aactcagaga ggcattgccg toattccaaa atcttccaag 840  
 aaggaaaggt tacttggcaa cctagaaatc gaaaaaaagt tcaatttaac ggagcaagaa 900  
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 gatggtaaat tccccacttt tgccctga 987

<210> 50  
 <211> 328  
 <212> PRT  
 <213> Artificial Sequence (isoleucine added at position 2)  
 <400> 50

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 20 25 30  
 Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys  
 35 40 45  
 Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile  
 50 55 60  
 Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu  
 65 70 75 80  
 Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys  
 85 90 95  
 Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His  
 100 105 110  
 Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro  
 115 120 125  
 Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu  
 130 135 140  
 Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val  
 145 150 155 160  
 Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser  
 165 170 175

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
 180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
 195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
 210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
 225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
 245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
 260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
 275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
 290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
 305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala  
 325

<210> 51  
 <211> 987  
 <212> DNA  
 <213> Artificial Sequence

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 tatcgctgtg tcgacggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180  
 cgtaaagcta tctctgaagg tctggtatct cgtaaggata tctttgtagt atctaagctg 240  
 tggaacaact ttcacacccc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300  
 atgggtctgg attatctgga tctgtactat atccactttc cgatcgcat taaatacgtg 360  
 cggttcgaag aaaaatatcc gccgggcttt tacactgggtg cagacgacga aaagaagggt 420  
 cacatcactg aagctcacgt accgatcatc gacacttacc gtgctctgga ggaatgtgta 480  
 gacgaaggtc tgatcaaata tatcggtgta tctaacttcc agggttctct gatccaggat 540  
 ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600  
 acccaggaac acctgggttg attctgcaaa ctgcacgata tccaagtagt agcatactct 660  
 tctttcggtc cgcagttctt catcgaaatg gacctgcagc tggctaagac caccctgact 720  
 ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccgggctc tactacctct 780



Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
 245 250 255  
 Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
 260 265 270  
 Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
 275 280 285  
 Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
 290 295 300  
 Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
 305 310 315 320  
 Asp Gly Lys Phe Pro Thr Phe Ala  
 325

<210> 53  
 <211> 1461  
 <212> DNA  
 <213> Sus scrofa

<400> 53  
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 <211> 487  
 <212> PRT  
 <213> Artificial Sequence

<400> 56

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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Pro Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg  
 355 360 365  
 Met Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln  
 370 375 380  
 Leu Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu  
 385 390 395 400  
 Val Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly  
 405 410 415  
 Ser Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg  
 420 425 430  
 Lys Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg  
 435 440 445  
 Phe Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala  
 450 455 460  
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 Gly Lys Ala Glu Ile Lys Ser  
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<210> 57  
 <211> 1098  
 <212> DNA  
 <213> Candida boidinii

<400> 57  
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<210> 58  
<211> 365  
<212> PRT  
<213> Candida boidinii

<400> 58

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20 25 30  
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35 40 45  
Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
50 55 60  
Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
65 70 75 80  
Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
85 90 95  
Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
100 105 110  
Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
115 120 125  
Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
130 135 140  
Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
145 150 155 160  
Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
165 170 175  
Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
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Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
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Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
210 215 220















<400> 64

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Gly	Pro	Asn	Leu	Glu	Pro	Pro	Thr	Asp	Cys	Glu	Ile	Leu	Asp	Gly	Ser	
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Gly	Gln	Tyr	Leu	Met	Pro	Gly	Gly	Ile	Asp	Pro	His	Thr	His	Met	Gln	
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Leu	Pro	Phe	Met	Gly	Thr	Val	Ala	Ser	Glu	Asp	Phe	Phe	Ser	Gly	Thr	
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Ala	Ala	Gly	Leu	Ala	Gly	Gly	Thr	Thr	Ser	Ile	Ile	Asp	Phe	Val	Ile	
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Pro	Asn	Pro	Gln	Gln	Ser	Leu	Leu	Glu	Ala	Phe	His	Thr	Trp	Arg	Gly	
			100					105						110		
Trp	Ala	Gln	Lys	Ser	Ala	Ser	Asp	Tyr	Gly	Phe	His	Val	Ala	Ile	Thr	
		115					120					125				
Trp	Trp	Ser	Glu	Gln	Val	Ala	Glu	Glu	Met	Gly	Glu	Leu	Val	Ala	Lys	
	130					135					140					
His	Gly	Val	Asn	Ser	Phe	Lys	His	Phe	Met	Ala	Tyr	Lys	Asn	Ala	Ile	
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Met	Ala	Ala	Asp	Asp	Thr	Leu	Val	Ala	Ser	Phe	Glu	Arg	Cys	Leu	Gln	
				165					170					175		
Leu	Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	
			180					185					190			
His	Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	
		195					200					205				
His	Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	
	210					215					220					
Ala	Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	
225					230					235					240	
Ile	Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	
				245					250					255		
Gly	Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	
			260					265					270			
Asp	Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	
		275					280					285				
Met	Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	
	290					295					300					
Gly	Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	

















Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	38.5	12.5	25	65	0.5	3.0	0.95
Gender	1.2	0.4	1	2	0.1	1.5	0.98
Marital Status	1.5	0.5	1	3	0.2	1.8	0.97
Education	12.5	2.5	9	16	0.3	2.2	0.96
Income	1500	500	1000	2500	0.4	2.5	0.95
Occupation	1.8	0.6	1	3	0.1	1.6	0.98
Health Status	1.2	0.4	1	2	0.1	1.5	0.98
Stress Level	2.5	1.0	1	4	0.2	1.8	0.97
Life Satisfaction	3.5	1.5	1	5	0.3	2.2	0.96
Resilience	2.8	1.2	1	4	0.2	1.8	0.97
Emotional Stability	3.2	1.0	1	4	0.1	1.6	0.98
Physical Health	3.8	1.2	1	5	0.2	1.8	0.97
Mental Health	3.0	1.0	1	4	0.1	1.6	0.98
Social Support	2.5	1.0	1	4	0.2	1.8	0.97
Life Events	1.5	0.5	1	3	0.1	1.5	0.98
Personal Growth	3.0	1.0	1	4	0.2	1.8	0.97
Life Purpose	3.5	1.2	1	5	0.3	2.2	0.96
Life Meaning	3.8	1.5	1	5	0.4	2.5	0.95
Life Satisfaction (Total)	3.5	1.5	1	5	0.3	2.2	0.96

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
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Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
35 40 45

Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr  
50 55 60

Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
65 70 75 80

Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala  
85 90 95

Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
100 105 110

Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile  
115 120 125

Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
130 135 140

Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu  
145 150 155 160

Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
165 170 175

Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn  
180 185 190

Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
195 200 205

Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn  
210 215 220

Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
225 230 235 240

Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly  
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Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
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52

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<211> 852
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<213> Artificial Sequence
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<210> 72
<211> 1602
<212> DNA
<213> Saccharomyces cerevisiae
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<212> PRT
<213> Saccharomyces cerevisiae
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Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser Thr  
65 70 75 80



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Glu Tyr Tyr Ser Glu Leu Met Leu Gly Gly His Asn Arg Ile Ser Ile 420	425	430
His Asn Val Cys Glu Asp Ser Leu Leu Ala Thr Pro Leu Ile Ile Asp 435	440	445
Leu Leu Val Met Thr Glu Phe Cys Thr Arg Val Ser Tyr Lys Lys Val 450	455	460
Asp Pro Val Lys Glu Asp Ala Gly Lys Phe Glu Asn Phe Tyr Pro Val 465	470	475
Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro Gly 485	490	495
Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu Asn 500	505	510
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 <212> DNA  
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	180		185		190	
Ala Ala Asn Gln	Asp Glu Arg Ala	Asn Asn Cys Ile	Asn Leu Asp Glu			
	195		200		205	
Lys Gly Asn Val	Thr Thr Arg Gly	Lys Trp Thr His	Leu Gln Arg Ile			
	210		215		220	
Arg Arg Asp Ile	Gln Asn Phe Lys	Glu Glu Asn Ala	Leu Asp Lys Val			
	225		230		235	
Ile Val Leu Trp	Thr Ala Asn Thr	Glu Arg Tyr Val	Glu Val Ser Pro			
	245		250		255	
Gly Val Asn Asp	Thr Met Glu Asn	Leu Leu Gln Ser	Ile Lys Asn Asp			
	260		265		270	
His Glu Glu Ile	Ala Pro Ser Thr	Ile Phe Ala Ala	Ala Ser Ile Leu			
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Asp Glu Tyr Tyr	Ser Glu Leu Met	Leu Gly Gly His	Asn Arg Ile Ser			
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Asp Leu Leu Val	Met Thr Glu Phe	Cys Thr Arg Val	Ser Tyr Lys Lys			
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Val Asp Pro Val	Lys Glu Asp Ala	Gly Lys Phe Glu	Asn Phe Tyr Pro			
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Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro  
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Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr  
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Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr  
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Bui, Peter  
Hua, Ling

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1197

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 <211> 1032  
 <212> DNA  
 <213> Artificial Sequence

<400> 36  
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 aacggtttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagtctcg 120  
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttgga cgctaaatac 180  
 ccgggtcggt tcgaaaccgc tgttggtgaa gacatgctga aacaggtgc ttacgacgaa 240  
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300  
 tacgacgaag ttgttacccc ggctatcggt ggtaccctga acgctctgct tgctgctgct 360  
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccgtttccgc tctgatcccg 420  
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480  
 aaagctaaaa cctgcccga atccgaccg cagaaatccc tgtgggtata cgctgcatcc 540  
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc aacttcaact 600  
 ctgaacgctg tactgcaaaa ctacactatt ggactatct tcgatccgga aactcagtcc 660  
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720  
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggttg 780  
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta ctgctggtac tttcgattgg 840  
 aacaccgttc tggctacctt ccgtaaactg taccgctcca aaaccttccc ggctgacttc 900  
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960  
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020  
 gaaaccgctt aa 1032

<210> 37  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu  
 1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu



<210> 38  
 <211> 942  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 38  
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 attccagtgt tgggtttcgg cacttggcgt tccgttgaca ataaoggtta ccattctgta 120  
 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180  
 gaagaagttg gcagggctat taaagattcc ggagtcctc gtgaggaaat ttttattact 240  
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300  
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360  
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420  
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480  
 acggggcaaaa ctaaagccgt tgggtgtctct aatttttcta ttaacaacat taaagaatta 540  
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcatccattg 600  
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg gtattgttgt tgaagcctac 660  
 tcaccatttg ggagtgctaa tgctccttta ctaaaagagc aagcaattat tgatatggct 720  
 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780  
 gttgttctg ccaaatcggt taatcctgaa agaattgtat ccaattttaa gattttcact 840  
 ctgcctgagg atgatttcaa gactattagt aacctatcca aagtgcattg taaaagaga 900  
 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39  
 <211> 313  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 39

Met	Gly	Pro	Ala	Thr	Leu	Lys	Asn	Ser	Ser	Ala	Thr	Leu	Lys	Leu	Asn
1				5					10					15	
Thr	Gly	Ala	Ser	Ile	Pro	Val	Leu	Gly	Phe	Gly	Thr	Trp	Arg	Ser	Val
			20					25					30		
Asp	Asn	Asn	Gly	Tyr	His	Ser	Val	Ile	Ala	Ala	Leu	Lys	Ala	Gly	Tyr
		35					40					45			
Arg	His	Ile	Asp	Ala	Ala	Ala	Ile	Tyr	Leu	Asn	Glu	Glu	Glu	Val	Gly
	50					55					60				
Arg	Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Ile	Thr
65					70					75				80	



cgtctgggtc tggactacgt agacctgtac ctgatgcact ggccggtacc gctgaaaact 360  
gaccgtgtta ctgatggtaa cgttctgtgt attccgactc tggaagacgg tactgtagac 420  
atcgacacta aggaatggaa cttcatcaag acttgggaac tgatgcagga actgccgaaa 480  
actggtaaaa ctaaagcagt aggtgtttcc aacttctcta tcaacaacat caaagaactg 540  
ctggaatctc cgaacaacaa agtagtaccg gcaactaacc agatcgaaat ccaccgctg 600  
ctgccgcagg acgaactgat cgcattctgc aaagagaaag gtatcgtagt agaagcatac 660  
tctccgttcg gctctgcaaa cgcaccgctg ctgaaagaac aggcaatcat cgacatggca 720  
aagaaacacg gtgtagaacc ggcacagctg atcatctctt ggtctatcca gcgtggttac 780  
gtagtactgg caaaatctgt aaaccoggaa cgtatcgat ctaacttcaa aatcttcaact 840  
ctgccggaag acgacttcaa aactatctct aacctgtcca aagttcacgg tactaaacgt 900  
gtagtagaca tgaaatgggg ttctttcccg atcttcagtt aa 942

<210> 41  
<211> 939  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 41  
atgactgcta ctttacatga ttctacgaaa atcctttctc taaatactgg agcccaaact 60  
cctcaaatag gtttaggtac gtggcagctg aaagagaacg atgcttataa ggctgtttta 120  
accgctttga aagatggcta ccgacacatt gatactgctg ctatttaccg taatgaagac 180  
caagtgggtc aagccatcaa ggattcaggt gttcctcggg aagaaatctt tgttactaca 240  
aagttatggt gtacacaaca ccacgaacct gaagtagcgc tggatcaatc actaaagagg 300  
ttaggattgg actacgtaga cttatatattg atgcattggc ctgccagatt agatccagcc 360  
tacaacaaaa atgaagacat cttgagtgtg ccaacaaaga aggatgggtc tcgtgcagtg 420  
gatataacca attggaattt catcaaaacc tgggaattaa tgcaggaact accaaagact 480  
ggtaaaacta aggcggttgg agtctccaac ttttctataa ataacctgaa agatctatta 540  
gcatctcaag gtaataagct tacgccagct gctaaccaag tcgaaatata tccattacta 600  
cctcaagacg aattgattaa tttttgtaaa agtaaaggca ttgtggttga agcttattct 660  
ccgttaggta gtaccgatgc tccactattg aaggaaccgg ttatccttga aattgcgaag 720  
aaaaataacg ttcaaccogg acacgttggt attagctggc acgtccaaag aggttatggt 780  
gtcttgccaa aatctgtgaa tcccgatcga atcaaaacga acaggaaaat atttactttg 840  
tctactgagg actttgaagc tatcaataac atatcgaagg aaaagggcga aaaaagggtt 900  
gtacatccaa attgggtctcc tttcgaagta ttcaagtaa 939

<210> 42  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 42

Met	Pro	Ala	Thr	Leu	His	Asp	Ser	Thr	Lys	Ile	Leu	Ser	Leu	Asn	Thr
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Gly	Ala	Gln	Ile	Pro	Gln	Ile	Gly	Leu	Gly	Thr	Trp	Gln	Ser	Lys	Glu
		20						25					30		
Asn	Asp	Ala	Tyr	Lys	Ala	Val	Leu	Thr	Ala	Leu	Lys	Asp	Gly	Tyr	Arg
	35						40					45			
His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly	Gln
	50					55					60				
Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr	Thr
65					70					75					80
Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp	Gln
			85					90						95	
Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met	His
			100					105					110		
Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile	Leu
		115					120					125			
Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr	Asn
	130					135					140				
Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys	Thr
145					150					155				160	
Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn	Leu
				165					170					175	
Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala	Asn
			180					185					190		
Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn	Phe
	195						200					205			
Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly	Ser
	210					215					220				
Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala	Lys
225					230					235					240
Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val	Gln
			245						250					255	
Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile	Lys
			260					265					270		
Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala	Ile

275	280	285	
Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro Asn			
290	295	300	
Trp Ser Pro Phe Glu Val Phe Lys			
305	310		

<210> 43  
 <211> 942  
 <212> DNA  
 <213> Artificial Sequence

<400> 43  
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 atcccgcaaa tcggcctggg tacttggcaa tctaaagaaa acgacgcata caaggctggt 120  
 ctgactgctc tgaaggatgg ctatcgtcac attgatactg ctgctattta tcgtaacgag 180  
 gaccaggtag gtcaggcaat caaggactct ggcgttccgc gtgaggaaat cttcgtaact 240  
 accaaactgt ggtgcactca gcatcatgaa ccggaagtag cactggatca atctctgaag 300  
 cgtctggggtc tggactatgt tgatctgtac ctgatgcatt ggccggcgcg cctggacca 360  
 gcgtatatta aaaacgaaga tatcctgtct gttccgacta agaaagacgg ctctcgtgct 420  
 gttgacatca ctaactggaa cttcatcaag acctgggaac tgatgcagga actgccgaag 480  
 actggtaaaa ctaaagctgt tggcgtatct aacttctcca tcaacaacct gaaggacctg 540  
 ctggcatccc agggcaacaa gctgactccg gctgctaacc aagtagagat ccaccgctg 600  
 ctgccgcagg acgaactgat caacttctgt aaatctaaag gcattgtagt tgaagcatat 660  
 tctccgctgg gttctaccga tgcgccactg ctgaaagagc cggtaatcct ggagatcgcg 720  
 aagaaaaaca acgtacaacc aggtcatgta gtaatctctt ggacacgtaca gcgcggctac 780  
 gtagttctgc cgaagtctgt aaaccgggat cgtatcaaaa ctaaccgtaa aatctttacc 840  
 ctgtccaccg aagatttcga agcaatcaac aacatctcca aggaaaagg cgagaaacgt 900  
 gtagttcacc caaactgggtc cccgtttgaa gtattcaagt aa 942

<210> 44  
 <211> 313  
 <212> PRT  
 <213> Artificial Sequence

<400> 44

Met Gly Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn	
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Thr Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys	
20 25 30	
Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr	



35	40	45
Arg His Ile Asp Thr Ala	Ala Ile Tyr Arg Asn	Glu Asp Gln Val Gly
50	55	60
Gln Ala Ile Lys Asp Ser	Gly Val Pro Arg Glu	Glu Ile Phe Val Thr
65	70	75
Thr Lys Leu Trp Cys Thr	Gln His His Glu	Pro Glu Val Ala Leu Asp
	85	90
Gln Ser Leu Lys Arg Leu	Gly Leu Asp Tyr Val	Asp Leu Tyr Leu Met
	100	105
His Trp Pro Ala Arg Leu	Asp Pro Ala Tyr Ile	Lys Asn Glu Asp Ile
	115	120
Leu Ser Val Pro Thr Lys	Lys Asp Gly Ser Arg	Ala Val Asp Ile Thr
	130	135
Asn Trp Asn Phe Ile Lys	Thr Trp Glu Leu Met	Gln Glu Leu Pro Lys
	145	150
Thr Gly Lys Thr Lys Ala	Val Gly Val Ser Asn	Phe Ser Ile Asn Asn
	165	170
Leu Lys Asp Leu Leu Ala	Ser Gln Gly Asn Lys	Leu Thr Pro Ala Ala
	180	185
Asn Gln Val Glu Ile His	Pro Leu Leu Pro Gln	Asp Glu Leu Ile Asn
	195	200
Phe Cys Lys Ser Lys Gly	Ile Val Val Glu Ala	Tyr Ser Pro Leu Gly
	210	215
Ser Thr Asp Ala Pro Leu	Leu Lys Glu Pro Val	Ile Leu Glu Ile Ala
	225	230
Lys Lys Asn Asn Val Gln	Pro Gly His Val Val	Ile Ser Trp His Val
	245	250
Gln Arg Gly Tyr Val Val	Leu Pro Lys Ser Val	Asn Pro Asp Arg Ile
	260	265
Lys Thr Asn Arg Lys Ile	Phe Thr Leu Ser Thr	Glu Asp Phe Glu Ala
	275	280
Ile Asn Asn Ile Ser Lys	Glu Lys Gly Glu Lys	Arg Val Val His Pro
	290	295
Asn Trp Ser Pro Phe Glu	Val Phe Lys	
	305	310

<210> 45  
 <211> 1029  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 45  
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ttgaaggaag	actataaggt	catcggttct	gccagaagtc	aagaaaaggc	cgagaattta	120
acggaggcct	ttggtaacaa	cccaaaattc	tccatggaag	ttgtcccaga	catatctaag	180
ctggacgcat	ttgaccatgt	tttccaaaag	cacggcaagg	atatcaagat	agttctacat	240
acggcctctc	cattctgctt	tgatatcact	gacagtgaac	gcgattttatt	aattcctgct	300
gtgaacggtg	ttaagggaat	tctccactca	attaaaaaat	acgccgctga	ttctgtagaa	360
cgtgtagttc	tcacctcttc	ttatgcagct	gtgttcgata	tggcaaaaga	aaacgataag	420
tctttaacat	ttaacgaaga	atcctggaac	ccagctacct	gggagagttg	ccaaagtgac	480
ccagttaacg	cctactgtgg	ttctaagaag	tttgcctgaaa	aagcagcttg	ggaatttcta	540
gaggagaata	gagactctgt	aaaattcgaa	ttaactgcog	ttaaccagct	ttacgttttt	600
ggtccgcaa	tgtttgacaa	agatgtgaaa	aaacacttga	acacatcttg	cgaactcgtc	660
aacagcttga	tgcatttctc	accagaggac	aagataccgg	aactatttgg	tggatacatt	720
gatgttcgtg	atgttgcaaa	ggctcattta	gttgcccttc	aaaagaggga	aacaattgggt	780
caaagactaa	tcgtatcgga	ggccagattt	actatgcagg	atgttctcga	tatccttaac	840
gaagacttcc	ctgttctaaa	aggcaatatt	ccagtgggga	aaccaggttc	tggtgctacc	900
cataacaccc	ttggtgctac	tcttgataat	aaaaagagta	agaaattggt	aggtttcaag	960
ttcaggaact	tgaaagagac	cattgacgac	actgcctccc	aaattttaaa	atttgagggc	1020
agaatataa						1029

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<210> 46
<211> 342
<212> PRT
<213> Saccharomyces cerevisiae

<400> 46
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Met	Ser	Val	Phe	Val	Ser	Gly	Ala	Asn	Gly	Phe	Ile	Ala	Gln	His	Ile
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Val	Asp	Leu	Leu	Leu	Lys	Glu	Asp	Tyr	Lys	Val	Ile	Gly	Ser	Ala	Arg
			20					25					30		
Ser	Gln	Glu	Lys	Ala	Glu	Asn	Leu	Thr	Glu	Ala	Phe	Gly	Asn	Asn	Pro
		35					40					45			
Lys	Phe	Ser	Met	Glu	Val	Val	Pro	Asp	Ile	Ser	Lys	Leu	Asp	Ala	Phe
	50					55					60				
Asp	His	Val	Phe	Gln	Lys	His	Gly	Lys	Asp	Ile	Lys	Ile	Val	Leu	His
65					70					75				80	
Thr	Ala	Ser	Pro	Phe	Cys	Phe	Asp	Ile	Thr	Asp	Ser	Glu	Arg	Asp	Leu
				85					90					95	
Leu	Ile	Pro	Ala	Val	Asn	Gly	Val	Lys	Gly	Ile	Leu	His	Ser	Ile	Lys

[illegible]

<210> 47

<212> DNA

<400> 47

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ctgactgaag catttggtaa caacccgaag ttctctatgg aagtagtacc ggacatttct 180

aaactggacg cattcgacca cgtattccaa aagcacggta aggatatcaa gatcgtactg 240

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cacactgcat ctccattctg ttttgacatc actgattctg agcgcgacct gctgattccg      300
gctgttaacg gtgttaaagg tattctgcac totattaaga aatatgctgc tgattccgta      360
gaacgcgtag ttctgacttc ctcttatgct gcagtattcg atatggctaa agagaacgac      420
aaatccctga cttttaacga agaattcttg aaccgcgcta cctgggaatc ttgccagtct      480
gacccgggta acgcttattg tggctctaag aagtttgctg aaaaagctgc ttgggaattc      540
ctggaagaaa accgtgactc tgtaaagttc gagctgaccg ctgtaaaccg ggtatacgtt      600
tttggcccg c agatgttcga taaagatgta aagaagcacc tgaacacttc ctgtgaactg      660
gtaaactctc tgatgcacct gtctccagaa gataaaatcc cggagctggt cggcgggttac      720
atcgacgttc gtgacgtagc aaaagcacat ctggttagctt tccagaagcg tgagactatc      780
ggccagcgtc tgattgttcc cgaggctcgt ttcacccatgc aggatgttct ggatattctg      840
aacgaagact tcccgggtact gaaaggtaac attccgggtg gtaaaccagg ctctggtgca      900
actcataaca ctctgggtgc aactctggat aacaagaagt ctaagaaact gctggggtttt      960
aaattccgta acctgaaaga aactattgac gacactgcat ctcagatcct gaaattcgaa     1020
ggtcgcatct aa                                                                1032

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<210> 48
<211> 343
<212> PRT
<213> Artificial Sequence

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<400> 48

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Met Gly Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His
1          5          10          15
Ile Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala
20        25        30
Arg Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn
35        40        45
Pro Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala
50        55        60
Phe Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu
65        70        75        80
His Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp
85        90        95
Leu Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile
100       105       110
Lys Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser
115       120       125
Tyr Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr

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130	135	140
Phe Asn Glu Glu Ser Trp Asn Pro Ala Thr Trp Glu Ser Cys Gln Ser		
145	150	155 160
Asp Pro Val Asn Ala Tyr Cys Gly Ser Lys Lys Phe Ala Glu Lys Ala		
	165 170	175
Ala Trp Glu Phe Leu Glu Glu Asn Arg Asp Ser Val Lys Phe Glu Leu		
	180 185	190
Thr Ala Val Asn Pro Val Tyr Val Phe Gly Pro Gln Met Phe Asp Lys		
	195 200	205
Asp Val Lys Lys His Leu Asn Thr Ser Cys Glu Leu Val Asn Ser Leu		
	210 215	220
Met His Leu Ser Pro Glu Asp Lys Ile Pro Glu Leu Phe Gly Gly Tyr		
	225 230	235 240
Ile Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln Lys		
	245 250	255
Arg Glu Thr Ile Gly Gln Arg Leu Ile Val Ser Glu Ala Arg Phe Thr		
	260 265	270
Met Gln Asp Val Leu Asp Ile Leu Asn Glu Asp Phe Pro Val Leu Lys		
	275 280	285
Gly Asn Ile Pro Val Gly Lys Pro Gly Ser Gly Ala Thr His Asn Thr		
	290 295	300
Leu Gly Ala Thr Leu Asp Asn Lys Lys Ser Lys Lys Leu Leu Gly Phe		
	305 310	315 320
Lys Phe Arg Asn Leu Lys Glu Thr Ile Asp Asp Thr Ala Ser Gln Ile		
	325 330	335
Leu Lys Phe Glu Gly Arg Ile		
	340	

<210> 49  
 <211> 987  
 <212> DNA  
 <213> Artificial Sequence (isoleucine codon added)

<400> 49  
 atgatttcctt cactgggttac tcttaataac ggtctgaaaa tgccoctagt cggcttaggg 60  
 tgctggaaaa ttgacaaaaa agtctgtgcg aatcaaattt atgaagctat caaattaggc 120  
 taccgtttat tcgatggtgc ttgcgactac ggcaacgaaa aggaagttgg tgaaggtatc 180  
 aggaaagcca tctccgaagg tcttgtttct agaaaggata tatttgttgt ttcaaagtta 240  
 tggaacaatt ttcaccatcc tgatcatgta aaattagctt taaagaagac cttaaagcat 300  
 atgggacttg attatttaga cctgtattat attcaacttc caatgcctt caaatatggt 360  
 ccatttgaag agaaataccc tccaggattc tatacgggcg cagatgacga gaagaaaggt 420

cacatcaccg aagcacatgt accaatcata gatacgtacc gggctctgga agaattgtgtt 480  
 gatgaaggct tgattaagtc tattggtgtt tccaactttc aggggaagctt gattcaagat 540  
 ttattacgtg gttgtagaat caagcccggtg gctttgcaaa ttgaacaacca tccttatttg 600  
 actcaagaac acctagtgtga gttttgtaaa ttacacgata tccaagtagt tgcttactcc 660  
 tccttcgggtc ctcaatcatt cattgagatg gacttacagt tggcaaaaac cacgccaaact 720  
 ctgttcgaga atgatgtaat caagaagggtc tcacaaaacc atccaggcag taccacttcc 780  
 caagtattgc ttagatgggc aactcagaga ggcattgccg tcattccaaa atcttccaag 840  
 aaggaaaggt tacttggcaa cctagaaatc gaaaaaaagt tcactttaac ggagcaagaa 900  
 ttgaaggata tttctgcact aaatgccaac atcagattta atgatccatg gacctgggtg 960  
 gatggtaaatt tccccacttt tgcttga 987

<210> 50  
 <211> 328  
 <212> PRT  
 <213> Artificial Sequence (isoleucine added at position 2)  
 <400> 50

Met	Ile	Ser	Ser	Leu	Val	Thr	Leu	Asn	Asn	Gly	Leu	Lys	Met	Pro	Leu
1				5					10					15	
Val	Gly	Leu	Gly	Cys	Trp	Lys	Ile	Asp	Lys	Lys	Val	Cys	Ala	Asn	Gln
			20					25					30		
Ile	Tyr	Glu	Ala	Ile	Lys	Leu	Gly	Tyr	Arg	Leu	Phe	Asp	Gly	Ala	Cys
		35					40					45			
Asp	Tyr	Gly	Asn	Glu	Lys	Glu	Val	Gly	Glu	Gly	Ile	Arg	Lys	Ala	Ile
	50					55					60				
Ser	Glu	Gly	Leu	Val	Ser	Arg	Lys	Asp	Ile	Phe	Val	Val	Ser	Lys	Leu
65					70					75					80
Trp	Asn	Asn	Phe	His	His	Pro	Asp	His	Val	Lys	Leu	Ala	Leu	Lys	Lys
				85					90					95	
Thr	Leu	Ser	Asp	Met	Gly	Leu	Asp	Tyr	Leu	Asp	Leu	Tyr	Tyr	Ile	His
			100					105					110		
Phe	Pro	Ile	Ala	Phe	Lys	Tyr	Val	Pro	Phe	Glu	Glu	Lys	Tyr	Pro	Pro
		115					120					125			
Gly	Phe	Tyr	Thr	Gly	Ala	Asp	Asp	Glu	Lys	Lys	Gly	His	Ile	Thr	Glu
		130				135					140				
Ala	His	Val	Pro	Ile	Ile	Asp	Thr	Tyr	Arg	Ala	Leu	Glu	Glu	Cys	Val
145					150					155					160
Asp	Glu	Gly	Leu	Ile	Lys	Ser	Ile	Gly	Val	Ser	Asn	Phe	Gln	Gly	Ser
			165						170					175	

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala  
325

<210> 51  
<211> 987  
<212> DNA  
<213> Artificial Sequence

<400> 51  
atgggctctt ctctggtaac tctgaacaac ggtctgaaaa tgccgctggt aggcctgggc 60  
tgctggaaaa tcgataagaa agtatgtgct aaccaaattt atgaggctat caaactgggc 120  
tatagcctgt tcgacgggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180  
cgtaaagcta tctctgaagg tctggatatc cgtaaggata tctttgtagt atctaagctg 240  
tggaacaact ttcataccccc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300  
atgggtcttg attatctgga tctgtactat atccactttc cgatcgcatt taaatacgta 360  
ccgttcgaag aaaaatatcc gccgggcttt tacactgggtg cagacgacga aaagaagggt 420  
cacatcactg aagctcacgt accgatcatc gacacttacc gtgctctgga ggaatgtgta 480  
gacgaaggtc tgatcaaate tatcggtgta tctaacttcc agggttctct gatccaggat 540  
ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600  
aaccaggaac acctgggttg attctgcaaa ctgcacgata tccaagtagt agcatactct 660  
tctttcggtc cgcagtcttt catcgaaatg gacctgcagc tggctaagac caccgccgact 720  
ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccgggctc tactacctct 780

caggctactgc tgcgttgggc tactcagcgt ggcacgcgtg ttatcccgaa atcttctaag 840  
aaagaacgctc tgctgggtaa cctggaaatc gaaaagaaat tcactctgac cgaacaggaa 900  
ctgaaagata tctctgctct gaacgctaac atccggtttca acgatccgtg gacctggctg 960  
gatggtaaata tcccgaacttt cgcttaa 987

<210> 52  
<211> 328  
<212> PRT  
<213> Artificial Sequence

<400> 52

Met Gly Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu  
1 5 10 15  
Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln  
20 25 30  
Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys  
35 40 45  
Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile  
50 55 60  
Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu  
65 70 75 80  
Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys  
85 90 95  
Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His  
100 105 110  
Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro  
115 120 125  
Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu  
130 135 140  
Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val  
145 150 155 160  
Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser  
165 170 175  
Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
180 185 190  
Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
195 200 205  
Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
210 215 220  
Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
225 230 235 240







Ile Pro Ser Asp Gly Lys Phe Ala Met Arg Ala Ser Ala Leu Gln Glu  
 210 215 220

Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Val Val  
 225 230 235 240

Ala Thr Leu Gly Thr Thr Ser Cys Cys Ser Phe Asp Asn Leu Leu Glu  
 245 250 255

Val Gly Pro Ile Cys His Glu Glu Asp Ile Trp Leu His Val Asp Ala  
 260 265 270

Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu Leu  
 275 280 285

Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys Trp  
 290 295 300

Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Arg Arg Thr  
 305 310 315 320

Asp Leu Thr Gly Ala Phe Lys Leu Asp Pro Val Tyr Leu Lys His Ser  
 325 330 335

His Gln Gly Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Leu Pro  
 340 345 350

Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg Met  
 355 360 365

Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln Leu  
 370 375 380

Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu Val  
 385 390 395 400

Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly Ser  
 405 410 415

Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg Lys  
 420 425 430

Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg Phe  
 435 440 445

Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala Trp  
 450 455 460

Glu His Ile Arg Gly Leu Ala Ala Glu Leu Leu Ala Ala Glu Glu Gly  
 465 470 475 480

Lys Ala Glu Ile Lys Ser  
 485

<210> 55  
 <211> 1464  
 <212> DNA  
 <213> Artificial Sequence

<400> 55  
 atgggtaacg cttccgattt ccgtcgtcgt ggcaaagaaa tggtagacta catggcagat



20							25					30				
Asp	Val	Gln	Pro	Gly	Tyr	Leu	Arg	Pro	Leu	Ile	Pro	Ala	Thr	Ala	Pro	
		35					40					45				
Gln	Glu	Pro	Asp	Thr	Phe	Glu	Asp	Ile	Leu	Gln	Asp	Val	Glu	Lys	Ile	
	50					55					60					
Ile	Met	Pro	Gly	Val	Thr	His	Trp	His	Ser	Pro	Tyr	Phe	Phe	Ala	Tyr	
65					70					75					80	
Phe	Pro	Thr	Ala	Ser	Ser	Tyr	Pro	Ala	Met	Leu	Ala	Asp	Met	Leu	Cys	
				85					90					95		
Gly	Ala	Ile	Gly	Cys	Ile	Gly	Phe	Ser	Trp	Ala	Ala	Ser	Pro	Ala	Cys	
			100					105					110			
Thr	Glu	Leu	Glu	Thr	Val	Met	Met	Asp	Trp	Leu	Gly	Lys	Met	Leu	Gln	
		115					120					125				
Leu	Pro	Glu	Ala	Phe	Leu	Ala	Gly	Glu	Ala	Gly	Glu	Gly	Gly	Gly	Val	
	130					135					140					
Ile	Gln	Gly	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Val	Ala	Leu	Leu	Ala	Ala	
145					150					155					160	
Arg	Thr	Lys	Val	Val	Arg	Arg	Leu	Gln	Ala	Ala	Ser	Pro	Gly	Leu	Thr	
				165					170					175		
Gln	Gly	Ala	Val	Leu	Glu	Lys	Leu	Val	Ala	Tyr	Ala	Ser	Asp	Gln	Ala	
			180					185					190			
His	Ser	Ser	Val	Glu	Arg	Ala	Gly	Leu	Ile	Gly	Gly	Val	Lys	Leu	Lys	
		195					200					205				
Ala	Ile	Pro	Ser	Asp	Gly	Lys	Phe	Ala	Met	Arg	Ala	Ser	Ala	Leu	Gln	
	210					215					220					
Glu	Ala	Leu	Glu	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Ile	Pro	Phe	Phe	Val	
225					230					235					240	
Val	Ala	Thr	Leu	Gly	Thr	Thr	Ser	Cys	Cys	Ser	Phe	Asp	Asn	Leu	Leu	
				245					250					255		
Glu	Val	Gly	Pro	Ile	Cys	His	Glu	Glu	Asp	Ile	Trp	Leu	His	Val	Asp	
			260					265					270			
Ala	Ala	Tyr	Ala	Gly	Ser	Ala	Phe	Ile	Cys	Pro	Glu	Phe	Arg	His	Leu	
		275					280					285				
Leu	Asn	Gly	Val	Glu	Phe	Ala	Asp	Ser	Phe	Asn	Phe	Asn	Pro	His	Lys	
	290					295					300					
Trp	Leu	Leu	Val	Asn	Phe	Asp	Cys	Ser	Ala	Met	Trp	Val	Lys	Arg	Arg	
305					310					315					320	
Thr	Asp	Leu	Thr	Gly	Ala	Phe	Lys	Leu	Asp	Pro	Val	Tyr	Leu	Lys	His	
				325					330					335		
Ser	His	Gln	Gly	Ser	Gly	Leu	Ile	Thr	Asp	Tyr	Arg	His	Trp	Gln	Leu	
			340					345					350			

Pro Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg  
 355 360 365  
 Met Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln  
 370 375 380  
 Leu Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu  
 385 390 395 400  
 Val Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly  
 405 410 415  
 Ser Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg  
 420 425 430  
 Lys Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg  
 435 440 445  
 Phe Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala  
 450 455 460  
 Trp Glu His Ile Arg Gly Leu Ala Ala Glu Leu Leu Ala Ala Glu Glu  
 465 470 475 480  
 Gly Lys Ala Glu Ile Lys Ser  
 485

<210> 57  
 <211> 1098  
 <212> DNA  
 <213> Candida boidinii

<400> 57  
 atgggtaaga ttgtcttagt tctttatgat gctggttaagc acgctgctga tgaagaaaaa 60  
 ttatatgggt gtactgaaaa taaattaggt attgctaatt ggtaaaaaga tcaaggcat 120  
 gaactaatta ctacttctga taaagaaggt gaaacaagtg aattggataa acatatccca 180  
 gatgctgata ttatcatcac cactcctttc catcctgctt atatcactaa ggaaagactt 240  
 gacaaggcta agaacttaaa attagtcgtt gtcgctggtg ttggttctga tcacattgat 300  
 ttagattata ttaatcaaac aggtaagaaa atctcagtc tggaagttac aggttcta 360  
 gttgtctctg ttgctgaaca cgttgctcatg accatgcttg tcttggttag aaatttcgtt 420  
 ccagcacatg aacaaattat taaccacgat tgggaggttg ctgctatcgc taaggatgct 480  
 tacgatatcg aaggtaaaac tatcgctacc attggtgctg gtagaattgg ttacagagtc 540  
 ttggaaagat tactcccatt taatccaaaa gaattattat actacgatta tcaagcttta 600  
 ccaaaagaag ctgaagaaaa agttggtgct agaagagttg aaaatattga agaattagtt 660  
 gctcaagctg atatcggttac agttaatgct ccattacacg caggtacaaa aggtttaatt 720  
 aataaggaat tattatctaa atttaaaaaa ggtgcttggt tagtcaatac cgcaagaggt 780  
 gctatttggtg ttgctgaaga tggtgcagca gctttagaat ctggtcaatt aagaggttac 840

ggtggtgatg tttggttccc acaaccagct ccaaaggatc acccatggag agatatgaga 900  
 aataaatatg gtgctggttaa tgccatgact cctcactact ctggtactac tttagacgct 960  
 caaacaagat acgctgaagg tactaaaaat attttggaaat cattctttac cggtaaat 1020  
 gattacagac cacaagatat tatcttatta aatggtgaat acgttactaa agcttacggt 1080  
 aaacacgata agaaataa 1098

<210> 58  
 <211> 365  
 <212> PRT  
 <213> Candida boidinii

<400> 58

Met	Gly	Lys	Ile	Val	Leu	Val	Leu	Tyr	Asp	Ala	Gly	Lys	His	Ala	Ala	1	5	10	15
Asp	Glu	Glu	Lys	Leu	Tyr	Gly	Cys	Thr	Glu	Asn	Lys	Leu	Gly	Ile	Ala	20	25	30	
Asn	Trp	Leu	Lys	Asp	Gln	Gly	His	Glu	Leu	Ile	Thr	Thr	Ser	Asp	Lys	35	40	45	
Glu	Gly	Glu	Thr	Ser	Glu	Leu	Asp	Lys	His	Ile	Pro	Asp	Ala	Asp	Ile	50	55	60	
Ile	Ile	Thr	Thr	Pro	Phe	His	Pro	Ala	Tyr	Ile	Thr	Lys	Glu	Arg	Leu	65	70	75	80
Asp	Lys	Ala	Lys	Asn	Leu	Lys	Leu	Val	Val	Val	Ala	Gly	Val	Gly	Ser	85	90	95	
Asp	His	Ile	Asp	Leu	Asp	Tyr	Ile	Asn	Gln	Thr	Gly	Lys	Lys	Ile	Ser	100	105	110	
Val	Leu	Glu	Val	Thr	Gly	Ser	Asn	Val	Val	Ser	Val	Ala	Glu	His	Val	115	120	125	
Val	Met	Thr	Met	Leu	Val	Leu	Val	Arg	Asn	Phe	Val	Pro	Ala	His	Glu	130	135	140	
Gln	Ile	Ile	Asn	His	Asp	Trp	Glu	Val	Ala	Ala	Ile	Ala	Lys	Asp	Ala	145	150	155	160
Tyr	Asp	Ile	Glu	Gly	Lys	Thr	Ile	Ala	Thr	Ile	Gly	Ala	Gly	Arg	Ile	165	170	175	
Gly	Tyr	Arg	Val	Leu	Glu	Arg	Leu	Leu	Pro	Phe	Asn	Pro	Lys	Glu	Leu	180	185	190	
Leu	Tyr	Tyr	Asp	Tyr	Gln	Ala	Leu	Pro	Lys	Glu	Ala	Glu	Glu	Lys	Val	195	200	205	
Gly	Ala	Arg	Arg	Val	Glu	Asn	Ile	Glu	Glu	Leu	Val	Ala	Gln	Ala	Asp	210	215	220	

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile  
 225 230 235 240  
 Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn  
 245 250 255  
 Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu  
 260 265 270  
 Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln  
 275 280 285  
 Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly  
 290 295 300  
 Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala  
 305 310 315 320  
 Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe  
 325 330 335  
 Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly  
 340 345 350  
 Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys  
 355 360 365

<210> 59  
 <211> 1098  
 <212> DNA  
 <213> Artificial Sequence

<400> 59  
 atgggcaaaa tcgttctggt tctgtatgac gctggtaa acgctgctga cgaagaaaaa 60  
 ctgtacggtt gcaccgaaaa caaactgggt atcgctaact ggctgaaaga tcagggtcac 120  
 gaactgatca ctacctctga caaagaaggt gaaacctctg aactggacaa acacatccccg 180  
 gatgcagata tcatcatcac cactccgttc caccggctt acatcaccaa agagcgtctg 240  
 gacaaagcta aaaacctgaa actggtagta gttgctggtg taggttctga ccacatcgac 300  
 ctggactaca tcaaccagac tggtaaaaaa atctctgtac tggaagtaac tggttctaac 360  
 gttgtttctg ttgctgaaca cgttgtaatg actatgctgg ttctggttcg taacttcgtt 420  
 ccggctcagc aacagatcat caaccacgat tgggaagttg cagcaatcgc taaagacgct 480  
 tatgacatcg aaggcaaaac catcgctact atcggcgctg gccgtatcgg ttaccgtggt 540  
 ctggaacgtc tgctgccgtt caaccgaaa gaactgctgt actacgacta ccaggctctg 600  
 ccgaaagaag cagaggagaa agttggtgct cgccgtgtag agaacatcga agagctggta 660  
 gctcaggctg acatcggttac tgttaacgct ccgctgcacg caggcactaa aggtctgatt 720  
 aacaagagc tgctgtctaa attcaaaaaa ggtgcatggc tggttaacac tgcacgtggg 780  
 gctatctgcg ttgctgaaga cgttgctgct gcaactggaat ctggtcagct gcgtgggttac 840



ggtggtgacg tatggtttcc gcagccggct ccgaaagatc acccgtggcg tgatatgcgt 900  
aacaaatatg gcgctggtaa cgcaatgacc ccgcactact ctggtaccac tctggatgct 960  
cagacccggt acgctgaagg tactaaaaac atcctggaat ctttcttcac tggtaaattc 1020  
gactaccgcc cgcaggacat cattctgctg aacgggtgaat atgtaactaa agcttacggc 1080  
aaacacgaca aaaaataa 1098

<210> 60  
<211> 365  
<212> PRT  
<213> Artificial Sequence

<400> 60

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala  
1 5 10 15  
Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala  
20 25 30  
Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys  
35 40 45  
Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
50 55 60  
Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
65 70 75 80  
Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
85 90 95  
Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
100 105 110  
Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
115 120 125  
Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
130 135 140  
Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
145 150 155 160  
Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
165 170 175  
Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
180 185 190  
Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
195 200 205  
Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
210 215 220  
Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile





Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	His	180	185	190
Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	His	195	200	205
Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	Ala	210	215	220
Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	Ile	225	230	235
Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	Gly	245	250	255
Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	Asp	260	265	270
Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	Met	275	280	285
Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	Gly	290	295	300
Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	Phe	305	310	315
Cys	Ala	Glu	Gln	Lys	Ala	Met	Gly	Arg	Asp	Asp	Phe	Ser	Arg	Ile	Pro	325	330	335
Asn	Gly	Thr	Ala	Gly	Ile	Glu	Asp	Arg	Met	Ala	Val	Leu	Trp	Asp	Ala	340	345	350
Gly	Val	Asn	Ser	Gly	Arg	Leu	Ser	Met	His	Glu	Phe	Val	Ala	Leu	Thr	355	360	365
Ser	Thr	Asn	Thr	Ala	Lys	Ile	Phe	Asn	Leu	Phe	Pro	Arg	Lys	Gly	Ala	370	375	380
Ile	Arg	Val	Gly	Ala	Asp	Ala	Asp	Leu	Val	Leu	Trp	Asp	Pro	Gln	Gly	385	390	395
Thr	Arg	Thr	Leu	Ser	Ala	Gln	Thr	His	His	Gln	Arg	Val	Asp	Phe	Asn	405	410	415
Ile	Phe	Glu	Gly	Arg	Thr	Val	Arg	Gly	Val	Pro	Ser	His	Thr	Ile	Ser	420	425	430
Gln	Gly	Lys	Val	Leu	Trp	Ala	Asp	Gly	Asp	Leu	Arg	Arg	Arg	Gly	Arg	435	440	445
Gly	Gly	Ala	Val	Cys	Gly	Thr	Ala	Gly	Val	Ser	Val	Gly	Val	Arg	Gly	450	455	460
Ala	Gly	Ala	Thr	Arg	Arg	Thr	Ala	Ala	Pro	Asp	Ala	Arg	Ser	Ala	Leu	465	470	475
Arg	Pro	Leu	Gly	Leu	Leu	Arg	Ser	Pro	Ser	Pro	Ala	Ser	Gln	Ile		485	490	495

<210> 63  
 <211> 1491  
 <212> DNA  
 <213> Artificial Sequence

<400> 63  
 atgggctctc tgctgatccg tgggtgctacc gttggttacc acgaagaatc ttatccgget 60  
 gacgtttctgt gcgttgacgg tctgatccgt gctatcggtc cgaacctgga accgccgacc 120  
 gactgcgaaa tcttggaagg ttctgggtcag tacctgatgc cgggtgggtat cgaccgcgat 180  
 actcacatgc agctgcggtt tatgggtact gttgcttctg aagacttctt ctctggcacc 240  
 gctgctgggc tggtgggtgg taccacctct atcatcgact tcgttatccc gaaccgcgag 300  
 cagtctctgc tggaagcttt ccataacttg cgtgggtggg ctcagaaatc tgcactctgac 360  
 tacggtttcc acgttgctat cacctgggtg tctgaacagg ttgctgaaga aatgggagaa 420  
 ctgggttgcta aacacggtgt taactcttcc aaacacttca tggcttataa aaacgcaatt 480  
 atggcgggtg acgacactct ggttgcttct ttcgaacgct gtctgcagct gggcgtggtt 540  
 ccgaccgttc acgtgaaaaa cggcgagctg gtttatcacc tgcagaaaaa actgctggct 600  
 cagggtatga ctggcccgga agctcaccgc ctgtctcgtc cgtctcaggt tgagggcgaa 660  
 gctgcttctc gtgctatccg tctcgctgaa accatcggtt ccccgctgta ttagtctcat 720  
 atctcttctc gtgaagctct ggatgagatt acttacgcac gtgctaaggg tcagccggtt 780  
 tacggtgaag ttctgcgggg tcatctgctg ctggatgatt ctgtataccg cgatccggac 840  
 tgggcaactg ctgctgggtt cgttatgtcc ccgccgttcc gtccgcgtga gcatcaggag 900  
 gcaactgtggc gcggcctgca gtctggtaac ctgcatacta ctgctactga tcaactgttg 960  
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<210> 64  
 <211> 496  
 <212> PRT  
 <213> Artificial Sequence



305                      310                      315                      320

Phe Cys Ala Glu Gln Lys Ala Met Gly Arg Asp Asp Phe Ser Arg Ile  
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Pro Asn Gly Thr Ala Gly Ile Glu Asp Arg Met Ala Val Leu Trp Asp  
                                 340                      345                      350

Ala Gly Val Asn Ser Gly Arg Leu Ser Met His Glu Phe Val Ala Leu  
                                 355                      360                      365

Thr Ser Thr Asn Thr Ala Lys Ile Phe Asn Leu Phe Pro Arg Lys Gly  
                                 370                      375                      380

Ala Ile Arg Val Gly Ala Asp Ala Asp Leu Val Leu Trp Asp Pro Gln  
385                                   390                      395                      400

Gly Thr Arg Thr Leu Ser Ala Gln Thr His His Gln Arg Val Asp Phe  
                                 405                      410                      415

Asn Ile Phe Glu Gly Arg Thr Val Arg Gly Val Pro Ser His Thr Ile  
                                 420                      425                      430

Ser Gln Gly Lys Val Leu Trp Ala Asp Gly Asp Leu Arg Arg Arg Gly  
                                 435                      440                      445

Arg Gly Gly Ala Val Cys Gly Thr Ala Gly Val Ser Val Gly Val Arg  
450                                   455                      460

Gly Ala Gly Ala Thr Arg Arg Thr Ala Ala Pro Asp Ala Arg Ser Ala  
465                                   470                      475                      480

Leu Arg Pro Leu Gly Leu Leu Arg Ser Pro Ser Pro Ala Ser Gln Ile  
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<210> 65  
<211> 1683  
<212> DNA  
<213> Penicillium simplicissimum

<400> 65  
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gaagtcgtcc ttgcgaatgg cgagcttctt aggactggca tgggggctct acctgatcct 660  
 aaacgtcccg aaacgatggg gctaaagcca gaagaccagc catggagcaa aatcgctcat 720  
 ctgtttcctt atggcttcgg tccctatata gatgggctat tcagccaatc gaatatggga 780  
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 ctaggcatgg cccctcaaaa tgttcccact attcgccaca ttcttttgga tgcagcgggtg 960  
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 aagatcgoga aacagctcaa cttgggaoga tggaactttt acggggcgct ctatggacct 1080  
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 gtcaagtttt attttcogga ggacactcct gaaaactccg ttctccgcgt gcgtgataag 1200  
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 aacagcagct tctaagggtt caatgaggtc ctcaagaatg cgtgggatcc taatggcatc 1620  
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 taa 1683

<210> 66  
 <211> 560  
 <212> PRT  
 <213> Penicillium simplicissimum

<400> 66

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			20					25					30		
Gly	Ser	Glu	Asn	Val	Glu	Val	Ile	Ser	Ser	Lys	Asp	Gln	Ile	Val	Asp
		35				40						45			
Gly	Ser	Tyr	Met	Lys	Pro	Thr	His	Thr	His	Asp	Pro	His	His	Val	Met
	50					55				60					
Asp	Gln	Asp	Tyr	Phe	Leu	Ala	Ser	Ala	Ile	Val	Ala	Pro	Arg	Asn	Val
65					70					75				80	





405	410	415
Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val Ser 420 425 430		
Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys Gln 435 440 445		
Glu Ala Gly Leu Asp Phe Ile Gly Thr Phe Thr Val Gly Met Arg Glu 450 455 460		
Met His His Ile Val Cys Ile Val Phe Asn Lys Lys Asp Leu Ile Gln 465 470 475 480		
Lys Arg Lys Val Gln Trp Leu Met Arg Thr Leu Ile Asp Asp Cys Ala 485 490 495		
Ala Asn Gly Trp Gly Glu Tyr Arg Thr His Leu Ala Phe Met Asp Gln 500 505 510		
Ile Met Glu Thr Tyr Asn Trp Asn Asn Ser Ser Phe Leu Arg Phe Asn 515 520 525		
Glu Val Leu Lys Asn Ala Val Asp Pro Asn Gly Ile Ile Ala Pro Gly 530 535 540		
Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu 545 550 555 560		

<210> 67  
 <211> 1686  
 <212> DNA  
 <213> Artificial Sequence

<400> 67  
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 ccgcaccacg ttatggacca ggactacttc ctgggttctg ctatcgttgc tccgcgtaac 240  
 gttgctgacg ttcagtctat cgttggtctg gctaacaaat tctctttccc gctgtggccg 300  
 atctctatcg gtcgtaactc tggttacggg ggtgctgctc cgcgtgtttc tggttctgtt 360  
 gttctggaca tgggtaaaaa catgaaccgt gttctggaag ttaacgttga aggtgcttac 420  
 tgcgttggtg aaccgggtgt aacttatcat gacctgcaca actacctgga agctaacaac 480  
 ctgcgtgaca aactgtggct ggacgtaccg gatctgggtg gtggttctgt tctgggtaac 540  
 gctgttgaaac gtggtgttg ttacaccccg tacggtgac attggatgat gcactctggc 600  
 atggaggtag tactggctaa cggtgaaact ctgcgtaccg gtatgggtgc tctgccggac 660  
 ccgaagcgtc cggaactat gggctctgaag ccggaggatc agccgtgggc taaaatcgct 720  
 catctgttcc cgtatggctt tggccgtac atcgacggtc tgttctctca gtctaacatg 780

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ggatcgtta ccaaaattgg catttggctg atgccgaacc cgggtgggta ccagtcttac      840
ctgattactc tgccgaaaga tggcgacctg aaacaggctg ttgatatacat tcgcccgtcg      900
cgtctgggta tggctctgca gaacgttccg actatccgcc acatcctgct ggacgtcgca      960
gtactgggtg acaaacgttc ctactcctct aaaactgaac cgctgtctga cgaagaactg     1020
gacaaaatcg ctaaacagct gaacctgggt cgttggaact tctacgggtgc tctgtacgggt     1080
ccggaaccga tccgtcgtgt tctgtgggag actatcaagg atgctttctc tgctatcccg     1140
ggtgttaaata tctacttccc ggaagacact ccgaaaaact ctgttctgcg tgtacgtgac     1200
aaaaccatgc agggatatccc gacctacgac gaactgaaat ggatcgactg gctgccgaac     1260
ggtgctcacc tgttcttttc tccgatcgct aaagtatccg gagaggacgc tatgatgcag     1320
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cagaagcgca aagttcagtg gctgatgcgt accctgatcg acgactgtgc tgctaacgggt     1500
tgggggtgaat accgtaccca cctggcattc atggaccaga tcatggaaac ctacaactgg     1560
aacaactctt ctttctgctg tttcaacgaa gttctgaaaa acgctgttga cccgaacgggt     1620
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ctgtaa                                           1686

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<210> 68
<211> 561
<212> PRT
<213> Artificial Sequence

<400> 68

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20          25          30

Val Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val
35          40          45

Asp Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val
50          55          60

Met Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn
65          70          75          80

Val Ala Asp Val Gln Ser Ile Val Gly Leu Ala Asn Lys Phe Ser Phe
85          90          95

Pro Leu Trp Pro Ile Ser Ile Gly Arg Asn Ser Gly Tyr Gly Gly Ala
100         105         110

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Ala	Pro	Arg	Val	Ser	Gly	Ser	Val	Val	Leu	Asp	Met	Gly	Lys	Asn	Met	
		115					120					125				
Asn	Arg	Val	Leu	Glu	Val	Asn	Val	Glu	Gly	Ala	Tyr	Cys	Val	Val	Glu	
	130					135					140					
Pro	Gly	Val	Thr	Tyr	His	Asp	Leu	His	Asn	Tyr	Leu	Glu	Ala	Asn	Asn	
	145				150					155					160	
Leu	Arg	Asp	Lys	Leu	Trp	Leu	Asp	Val	Pro	Asp	Leu	Gly	Gly	Gly	Ser	
			165						170					175		
Val	Leu	Gly	Asn	Ala	Val	Glu	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	
			180					185					190			
Asp	His	Trp	Met	Met	His	Ser	Gly	Met	Glu	Val	Val	Leu	Ala	Asn	Gly	
		195					200					205				
Glu	Leu	Leu	Arg	Thr	Gly	Met	Gly	Ala	Leu	Pro	Asp	Pro	Lys	Arg	Pro	
	210					215					220					
Glu	Thr	Met	Gly	Leu	Lys	Pro	Glu	Asp	Gln	Pro	Trp	Ser	Lys	Ile	Ala	
	225				230					235					240	
His	Leu	Phe	Pro	Tyr	Gly	Phe	Gly	Pro	Tyr	Ile	Asp	Gly	Leu	Phe	Ser	
				245					250					255		
Gln	Ser	Asn	Met	Gly	Ile	Val	Thr	Lys	Ile	Gly	Ile	Trp	Leu	Met	Pro	
			260					265					270			
Asn	Pro	Gly	Gly	Tyr	Gln	Ser	Tyr	Leu	Ile	Thr	Leu	Pro	Lys	Asp	Gly	
		275					280					285				
Asp	Leu	Lys	Gln	Ala	Val	Asp	Ile	Ile	Arg	Pro	Leu	Arg	Leu	Gly	Met	
	290					295					300					
Ala	Leu	Gln	Asn	Val	Pro	Thr	Ile	Arg	His	Ile	Leu	Leu	Asp	Ala	Ala	
	305				310					315					320	
Val	Leu	Gly	Asp	Lys	Arg	Ser	Tyr	Ser	Ser	Lys	Thr	Glu	Pro	Leu	Ser	
				325					330					335		
Asp	Glu	Glu	Leu	Asp	Lys	Ile	Ala	Lys	Gln	Leu	Asn	Leu	Gly	Arg	Trp	
			340					345					350			
Asn	Phe	Tyr	Gly	Ala	Leu	Tyr	Gly	Pro	Glu	Pro	Ile	Arg	Arg	Val	Leu	
		355					360					365				
Trp	Glu	Thr	Ile	Lys	Asp	Ala	Phe	Ser	Ala	Ile	Pro	Gly	Val	Lys	Phe	
	370					375					380					
Tyr	Phe	Pro	Glu	Asp	Thr	Pro	Glu	Asn	Ser	Val	Leu	Arg	Val	Arg	Asp	
	385				390					395					400	
Lys	Thr	Met	Gln	Gly	Ile	Pro	Thr	Tyr	Asp	Glu	Leu	Lys	Trp	Ile	Asp	
			405						410					415		
Trp	Leu	Pro	Asn	Gly	Ala	His	Leu	Phe	Phe	Ser	Pro	Ile	Ala	Lys	Val	
			420					425					430			
Ser	Gly	Glu	Asp	Ala	Met	Met	Gln	Tyr	Ala	Val	Thr	Lys	Lys	Arg	Cys	



<210> 70  
 <211> 283  
 <212> PRT  
 <213> Candida magnoliae

<400> 70

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala	
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			20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
	50					55					60					
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
65					70					75					80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
				85					90					95		
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
			100					105					110			
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
		115					120					125				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu	
	130					135					140					
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
145					150					155					160	
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser	
				165					170					175		
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn	
			180					185					190			
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195				200						205				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210					215					220					
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp	
225					230					235				240		
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
				245					250					255		
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
		260						265					270			
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro						

275

280

<210> 71  
<211> 852  
<212> DNA  
<213> Artificial Sequence

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tcttctctctg gtatcgggta cgtctctggc gaagcattcg ctcaggtagg tgctgacggt 180  
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gggtgttaaag ttaaagctta caaggctaac gtttcttctt ctgacgctgt aaaacagacc 300  
atcgaacagc agatcaaaga cttcgggtcac ctggacatcg ttgttgctaa cgctggtatc 360  
ccgtggacca aaggtgctta catcgaccag gacgacgata aacacttcga tcaggttggt 420  
gacgttgatc tgaaagggtg tgggttatgtt gctaaacacg ctggccgctc cttccgtgag 480  
cgtttcgaaa aggaaggtaa gaaaggcgct ctgggtttca ccgcttctat gtctgggtcac 540  
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tctctgggtac cgctggggcg tgggtggcgaa actgctgaac tgggtgggtg ttacctgttt 780  
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acctgccgt aa 852

<210> 72  
<211> 1602  
<212> DNA  
<213> *Saccharomyces cerevisiae*

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gctagtggcc gcttcgatgt aacgccact gttcaagact acgtgttcaa acttgacttg 180  
aaaaagccgg aaaaactagg aattatgctc attgggttag gtggcaacaa tggctccact 240  
ttagtggcct cggatttggc gaataagcac aatgtggagt ttcaaaactaa ggaaggcggt 300  
aagcaaccaa actacttcgg ctccatgact caatgttcta ccttgaaact gggatatgat 360  
gctggagggga atgacgttta tgctcctttt aactctctgt tgcccatggg tagcccaaac 420  
gactttgtcg tctctggttg ggacatcaat aacgcagatc tatacgaagc tatgcagaga 480

agtcaagttc tcgaatatga tctgcaacaa cgcttgaagg cgaagatgtc cttgggtgaag 540  
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 aactgcatca atttgatga aaaaggcaac gtaaccacga ggggtaagtg gacccatctg 660  
 caacgcatca gacgcgatat ccagaatttc aaagaagaaa acgcccttga taaagtaatc 720  
 gttcttttga ctgcaaatac tgagaggtac gtagaagtat ctcttggtgt taatgacacc 780  
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 gtcatacaat atatgaagcc cgtcggggac tcaaaagtgg caatggacga gtattacagt 1260  
 gagttgatgt taggtggcca taaccggatt tccattcaca atgtttgcga agattcttta 1320  
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 aatggcttaa acaagcaaag aaccgcctta gaaaattttt taagattgtt gattggattg 1560  
 ccttctcaaa acgaactaag attcgaagag agattgttgt aa 1602

<210> 73  
 <211> 533  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 73

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			20					25					30		
Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	Thr
		35					40					45			
Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	Glu
	50					55					60				
Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	Thr
65					70					75				80	





405                      410                      415  
 Glu Tyr Tyr Ser Glu Leu Met Leu Gly Gly His Asn Arg Ile Ser Ile  
                          420                      425                      430  
 His Asn Val Cys Glu Asp Ser Leu Leu Ala Thr Pro Leu Ile Ile Asp  
                          435                      440                      445  
 Leu Leu Val Met Thr Glu Phe Cys Thr Arg Val Ser Tyr Lys Lys Val  
                          450                      455                      460  
 Asp Pro Val Lys Glu Asp Ala Gly Lys Phe Glu Asn Phe Tyr Pro Val  
                          465                      470                      475                      480  
 Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro Gly  
                          485                      490                      495  
 Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu Asn  
                          500                      505                      510  
 Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg Phe  
                          515                      520                      525  
 Glu Glu Arg Leu Leu  
                          530

<210> 74  
 <211> 1605  
 <212> DNA  
 <213> Artificial Sequence

<400> 74  
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 acttacaaag acaacgaact gctgactaaa tactcttacg aaaacgctgt agtaactaaa 120  
 actgcttctg gtcgtttcga tgttactccg actgttcagg actacgtatt caaactggat 180  
 ctgaagaaac cggaaaagct gggtatcatg ctgatcggcc tgggtggtaa caacggctct 240  
 actctgggtg catctgttct ggcaaacaaa cacaacgtag aattccagac taaggaaggt 300  
 gttaaacagc cgaactactt tggttctatg actcagtgtt ctactctgaa gctgggcatt 360  
 gatgctgaag gtaacgacgt ttacgctccg ttcaactctc tgctgccgat ggtatctccg 420  
 aacgacttcg ttgtttctgg ttgggatatc aacaacgcgg atctgtacga agcaatgcag 480  
 cgttctcagg ttctggaata tgatctgcaa cagcgtctga aggctaagat gtctctgggt 540  
 aagccactgc cgtccatcta ctaccggat tttatcgcag ctaaccagga cgaacgtgct 600  
 aacaactgta tcaacctgga cgaaaagggg aacgttacta cccgtggtaa gtggactcac 660  
 ctgcagcgta tccgtcgtga tatccagaac ttcaaagagg aaaacgcact ggacaaagtt 720  
 atcgtactgt ggactgctaa cactgaacgt tacgtagaag tatccccggg tgtaaacgat 780  
 actatggaaa acctgctgca atctatcaag aacgaccacg aggaaatcgc tccgtccacc 840  
 atcttcgctg ctgcatctat cctggaaggc gtaccgtaca tcaacggctc tccgcagaac 900

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actttcgtac cgggtctggt acagctggct gaacacgaag gtaccttcat cgctggtgac 960
gatctgaaat ctggccagac taaactgaaa tctgtactgg cacagttcct ggttgacgct 1020
ggtatcaaac cggtttctat cgcttcttat aaccacctgg gtaacaacga cggctacaac 1080
ctgtctgctc cgaaacagtt ccgttctaaa gaaatctcta aatcctctgt aatcgacgac 1140
atcatcgctt ctaacgacat cctgtacaac gacaaaactgg gtaagaaagt agatcactgt 1200
atcgttatca aatacatgaa accggttggg gattctaaag ttgctatgga cgaatactac 1260
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tcttacaaga aagttgaccc ggttaaagaa gatgctggca aattcgaaaa cttctacccg 1440
gttctgacct tctgtcttta ctggctgaaa gctccgctga ctggtccagg cttccacccg 1500
gttaacggtc tgaacaaaca gcgtaccgct ctggaaaact tctgctgtct gctgatcggc 1560
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<210> 75
<211> 534
<212> PRT
<213> Artificial Sequence
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<400> 75
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Thr Asp Lys Cys Thr Tyr Lys Asp Asn Glu Leu Leu Thr Lys Tyr Ser
20 25 30
Tyr Glu Asn Ala Val Val Thr Lys Thr Ala Ser Gly Arg Phe Asp Val
35 40 45
Thr Pro Thr Val Gln Asp Tyr Val Phe Lys Leu Asp Leu Lys Lys Pro
50 55 60
Glu Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser
65 70 75 80
Thr Leu Val Ala Ser Val Leu Ala Asn Lys His Asn Val Glu Phe Gln
85 90 95
Thr Lys Glu Gly Val Lys Gln Pro Asn Tyr Phe Gly Ser Met Thr Gln
100 105 110
Cys Ser Thr Leu Lys Leu Gly Ile Asp Ala Glu Gly Asn Asp Val Tyr
115 120 125
Ala Pro Phe Asn Ser Leu Leu Pro Met Val Ser Pro Asn Asp Phe Val
130 135 140
Val Ser Gly Trp Asp Ile Asn Asn Ala Asp Leu Tyr Glu Ala Met Gln
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145		150		155		160
Arg Ser Gln Val	Leu Glu Tyr Asp	Leu Gln Gln Arg	Leu Lys Ala Lys			
	165		170		175	
Met Ser Leu Val	Lys Pro Leu Pro	Ser Ile Tyr Tyr	Pro Asp Phe Ile			
	180	185	190			
Ala Ala Asn Gln	Asp Glu Arg Ala	Asn Asn Cys Ile	Asn Leu Asp Glu			
	195	200	205			
Lys Gly Asn Val	Thr Thr Arg Gly	Lys Trp Thr His	Leu Gln Arg Ile			
	210	215	220			
Arg Arg Asp Ile	Gln Asn Phe Lys	Glu Glu Asn Ala	Leu Asp Lys Val			
225	230	235	240			
Ile Val Leu Trp	Thr Ala Asn Thr	Glu Arg Tyr Val	Glu Val Ser Pro			
	245	250	255			
Gly Val Asn Asp	Thr Met Glu Asn	Leu Leu Gln Ser	Ile Lys Asn Asp			
	260	265	270			
His Glu Glu Ile	Ala Pro Ser Thr	Ile Phe Ala Ala	Ala Ser Ile Leu			
	275	280	285			
Glu Gly Val Pro	Tyr Ile Asn Gly	Ser Pro Gln Asn	Thr Phe Val Pro			
	290	295	300			
Gly Leu Val Gln	Leu Ala Glu His	Glu Gly Thr Phe	Ile Ala Gly Asp			
305	310	315	320			
Asp Leu Lys Ser	Gly Gln Thr Lys	Leu Lys Ser Val	Leu Ala Gln Phe			
	325	330	335			
Leu Val Asp Ala	Gly Ile Lys Pro	Val Ser Ile Ala	Ser Tyr Asn His			
	340	345	350			
Leu Gly Asn Asn	Asp Gly Tyr Asn	Leu Ser Ala Pro	Lys Gln Phe Arg			
	355	360	365			
Ser Lys Glu Ile	Ser Lys Ser Ser	Val Ile Asp Asp	Ile Ile Ala Ser			
370	375	380				
Asn Asp Ile Leu	Tyr Asn Asp Lys	Leu Gly Lys Lys	Val Asp His Cys			
385	390	395	400			
Ile Val Ile Lys	Tyr Met Lys Pro	Val Gly Asp Ser	Lys Val Ala Met			
	405	410	415			
Asp Glu Tyr Tyr	Ser Glu Leu Met	Leu Gly Gly His	Asn Arg Ile Ser			
	420	425	430			
Ile His Asn Val	Cys Glu Asp Ser	Leu Leu Ala Thr	Pro Leu Ile Ile			
	435	440	445			
Asp Leu Leu Val	Met Thr Glu Phe	Cys Thr Arg Val	Ser Tyr Lys Lys			
	450	455	460			
Val Asp Pro Val	Lys Glu Asp Ala	Gly Lys Phe Glu	Asn Phe Tyr Pro			
465	470	475	480			

Val Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro  
 485 490 495  
 Gly Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu  
 500 505 510  
 Asn Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg  
 515 520 525  
 Phe Glu Glu Arg Leu Leu  
 530

<210> 76  
 <211> 2043  
 <212> DNA  
 <213> Hypomyces rosellus

<400> 76  
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 gtccctcaca aggccgtagg aactggaatt cctgaaggga gtcttcagtt cctgagcctt 120  
 cgagcctcag cacctatcgg aagcgccatt totcgcaaca actgggcccgt cacttgcgac 180  
 agtgacacagt cgggaaatga atgcaacaag gccattgatg gcaacaagga taccttttgg 240  
 cacacattct atggcgccaa cggggatcca aagccccctc acacatacac gattgacatg 300  
 aagacaactc agaacgtcaa cggcttgtct atgctgcctc gacaggatgg taaccaaacc 360  
 ggctggatcg gtcgccatga ggtttatcta agctcagatg gcacaaactg gggcagccct 420  
 gttgcgtcag gtagttgggt cgccgactct actacaaaat actccaactt tgaaactcgc 480  
 cctgctcgct atgttcgtct tgcgctatc actgaagcga atggccagcc ttggactagc 540  
 attgcagaga tcaacgtctt ccaagctagt tcttacacag cccccagcc tggctttgga 600  
 cgctgggggc cgactattga cttaccgatt gttcctgcgg ctgcagcaat tgaaccgaca 660  
 tcgggacgag tccttatgtg gtcttcatat cgcaatgatg catttgagg atccctgggt 720  
 ggtatcactt tgacgtcttc ctgggatcca tccactggta ttgtttccga cgcactgtg 780  
 acagtcacca agcatgatat gttctgccct ggtatctcca tggatggtaa cggtcagatc 840  
 gtagtcacag gtggcaacga tgccaagaag accagtttgt atgattcatc tagcgatagc 900  
 tggatcccgg gacctgacat gcaagtggct cgtgggtatc agtcatcagc taccatgtca 960  
 gacggtcgtg tttttacat tggaggctcc tggagcgggt gcgtatttga gaagaatggc 1020  
 gaagtctata gcccatcttc aaagacatgg acgtccctac ccaatgcca ggtcaacca 1080  
 atgttgacgg ctgacaagca aggattgtac cgttcagaca accacgcgtg gctctttgga 1140  
 tggaagaagg gttcgggtgtt ccaagcggga cctagcacag ccatgaactg gtactatacc 1200  
 agtggaagtg gtgatgtgaa gtcagccgga aaacgccagt ctaaccgtgg ttagccct 1260

gatgccatgt goggaaacgc tgtcatgtac gacgccgtta aaggaaagat cctgaccttt 1320  
 ggcggtccc cagattatca agactctgac gccacaacca acgcccacat catcaccctc 1380  
 ggtgaaccog gaacatctcc caacactgtc tttgctagca atgggttgta ctttgcccga 1440  
 acgtttcaca cctctgttgt tttccagac ggaagcacgt ttattacagg aggccaacga 1500  
 cgtggaattc cgttcgagga ttcaaccccg gtatttacac ctgagatcta cgtccctgaa 1560  
 caagacactt tctacaagca gaaccccaac tccattgttc gcgtctacca tagcatttcc 1620  
 cttttgttac ctgatggcag ggtatttaac ggtggtggtg gtctttgtgg cgattgtacc 1680  
 acgaatcatt togaogcgca aatctttacg ccaaactatc tttacaatag caacggcaat 1740  
 ctgcgcacac gtcccaagat taccagaacc tctacacaga gcgtcaaggt cggtggcaga 1800  
 attacaatct cgacggattc ttcgattagc aaggcgctgt tgattcgcta tggtacagcg 1860  
 acacacacgg ttaatactga ccagcgccgc attcccttga ctctgacaaa caatggagga 1920  
 aatagctatt ctttccaagt tctagcgac tctggtgttg ctttgccctgg ctactggatg 1980  
 ttgttcgtga tgaactcggc cgggtgttct agtgtggctt cgacgattcg cgttactcag 2040  
 tga 2043

<210> 77  
 <211> 680  
 <212> PRT  
 <213> *Hypomyces rosellus*  
 <400> 77

Met Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala  
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 Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro Glu  
 20 25 30  
 Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser  
 35 40 45  
 Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser  
 50 55 60  
 Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp  
 65 70 75 80  
 His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr  
 85 90 95  
 Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu  
 100 105 110  
 Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val  
 115 120 125  
 Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser Gly



Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg  
 465 470 475 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr  
 485 490 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe  
 500 505 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn  
 515 520 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro  
 530 535 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr  
 545 550 555 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn  
 565 570 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr  
 580 585 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser  
 595 600 605

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val  
 610 615 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly  
 625 630 635 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro  
 645 650 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val  
 660 665 670

Ala Ser Thr Ile Arg Val Thr Gln  
 675 680

<210> 78  
 <211> 2046  
 <212> DNA  
 <213> Artificial Sequence

<400> 78  
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 ctgctgtgctt ctgctccgat cggttctgct atctctcgta acaactgggc agttacctgc 180  
 gactccgcac agtctggtaa cgaatgcaac aaagctatcg acgtaacaa agacactttt 240  
 tggcacactt tctatggcgc taacggcgac ccgaaaccgc cgcacaccta caccatcgat 300  
 atgaaaacca ctcagaacgt aaacggcctg tctatgctgc cgcgccagga tggttaaccag 360







Gly Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met  
 305 310 315 320  
 Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val  
 325 330 335  
 Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr  
 340 345 350  
 Ser Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln  
 355 360 365  
 Gly Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys  
 370 375 380  
 Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr  
 385 390 395 400  
 Thr Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn  
 405 410 415  
 Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp  
 420 425 430  
 Ala Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln  
 435 440 445  
 Asp Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro  
 450 455 460  
 Gly Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala  
 465 470 475 480  
 Arg Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile  
 485 490 495  
 Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val  
 500 505 510  
 Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln  
 515 520 525  
 Asn Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu  
 530 535 540  
 Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys  
 545 550 555 560  
 Thr Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr  
 565 570 575  
 Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser  
 580 585 590  
 Thr Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser  
 595 600 605  
 Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr  
 610 615 620

